

4
SEQUENCE LISTING

96 AUG -9 AM 4:49

(1) GENERAL INFORMATION:

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.
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(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/599,974
(B) FILING DATE: 14-FEB-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/586,594
(B) FILING DATE: 16-JAN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-162 CP1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
CODING REGION: 1-2682

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGATGTGTC AGAAAATTCTA TGTGGTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACCTTAACC TGGCATATCC AATCTCTCCC TGGAAATTAA AGTTGTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAAATGC CTCGGCTTG	180
AAGGGGGCTT CTGAAGCAAT TGTGAGCT AAATTAATT CAAGTGGTAT CTACGTTCC	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGAATG AGCAAGGTCA AACTGCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTGCGCTC TGCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTG TGAAACCCGA TCCACCCCTA	720
GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTAAAGA TTTCTTGGGA CAGCCAAACA	780
ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA	840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT	900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG	960
AGTCACCTC AAGTCTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT	1020
AGTGTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC	1080
TCAAAACAGA TAGTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC	1140
ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA	1200
GGGAAGTTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT	1260

GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGGCCA	AAAACCTGCGT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACTT	1560
GAACCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTTGGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGGAAA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTCAAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTCGC	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGAC	GTTACTAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TCCCTTGTGA	ATTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2160
TCACTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGTCACTCC	TTCCCTGGAC	ACTGTCACCT	2220
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2280
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGA	TAATTTATT	2340
CCCATCGAGA	AATATCAGTT	TAGTCTTAC	CCAGTATTTA	TGGAAGGAGT	TGGAAAACCA	2400
AAGATAATT	ATGGTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2460
TATGTCATTG	TACCCATAAT	TATTCCTCT	TGTGTCTAC	TGCTCGGAAC	ACTGTTAATT	2520
TCACACCAGA	GAATGAAAAA	GTTGTTTG	GACGATGTT	CAAACCCAA	GAATTGTTCC	2580
TGGGCACAAG	GACTGAATT	CCAAAAGAGA	ACGGACACTC	TTTGAAGTCT	CTCATGACCA	2640
CTACAGATGA	ACCCAATCTA	CCAACCTCCC	AACAGTCCAT	ACAATATTAG	AAGATGTTA	2700
CATTGGATG	GAGGGAAACA	ACCCTAAACT	ATGGTTTGAA	TGACTAAGAA	ATAACATTTG	2760
A						2821

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
35 40 45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
50 55 60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65 70 75 80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
85 90 95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
100 105 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
115 120 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
130 135 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
145 150 155 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
165 170 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
180 185 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu

195 200 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
290 295 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
305 310 315 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
325 330 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
355 360 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
370 375 380

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
385 390 395 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
405 410 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
420 425 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
435 440 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465 470 475 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
485 490 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
500 505 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
515 520 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
530 535 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
545 550 555 560

Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
565 570 575

Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
580 585 590

Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
595 600 605

Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
610 615 620

Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625 630 635 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
645 650 655

Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
660 665 670

Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
675 680 685

Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
690 695 700

Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
705 710 715 720

Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
725 730 735

Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
740 745 750

Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
755 760 765

Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
770 775 780

Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
785 790 795 800

Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
805 810 815

Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp
820								825						830	
Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile
835							840					845			
Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg
850						855					860				
Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser
865					870					875			880		
Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Arg	Thr	Asp	Thr	Leu		
					885					890					

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
CODING REGION: 1349-2845

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA	GTGCCAACGG	GAAGGCTTAA	TTAACCTTG	GAANTGAGTC	CGAAGAGTCT	60
GGAAGTNTGT	AAGATGGAAG	ATACTATACA	AGATACTTCA	GAGCTGTACA	TTCTTCCAGG	120
GATGTAGGCT	AGCAGTTATT	TCATTAGTAT	ATGTCTATTT	TAGAATGGGA	AGAATTAGGA	180
AGATGAATGG	AGCCTGTGTC	TTTCACTACT	CTCCCAGGAG	GTTCCAGAAT	AGCNAAGTG	240
TCAGCCAGAA	TTCTTGAAGT	CATAGACTGG	AGTTAGAGAT	GAACATAAGC	TCATGTTAAG	300
CCTGGGTTAC	TTCTTATCAT	CCTTAATTTC	GAAAGCTAAG	AGGGCCTAAC	CATCAAGAAC	360
GTCCTGGAGG	AAAGAATGTT	TTAACGCCA	TTATTCAGTC	AAAGAAATTA	AGACTTGAGA	420
GAAATGCTCA	TTTCTCTCT	CATGATGGCT	CCTTACACCT	TACTTCTACC	GTACGATCCA	480
TGNGGCCCTA	CCCACGCAGG	ATACATGCAT	CTATATGAGA	GTGTCTNCCC	CTTCTAACTC	540

AGAGACTCTT GTTCTAGTCT GTGNTATAAA ATTCAGCTTG TGGAAGCTTT CTGAGGGGTT	600
GGCAGCATTG AATTTTACCT GCAATAGGTA AAGGTAATCT TTTGGGAAGT GAAGAGTGT	660
ATTAGACATT TCAGAAAGAA CAAACAGGAT TGGGGCTGCT ATGTGTTCTA CACAGGAATC	720
TTCCATAACA CAGAATAATT TATGTAGATA GAGACAAGAT GGAAATGCC AGGGCCCCAA	780
AATAGCCGCT GTTATTGTT AACCTCAAG GTTTCTGTT TGTTTATCTG TTTCTTGC	840
AGGATCATCT TCCAAGCACA TCCTGGGGA ACAGTGGCAG AGTCACTCGA GTTCATGAAA	900
CTATGGTGAC ATCTGAGCTT CCTTGGTTCT TCACAGAACAA TAAGCAGTTC CTTTGCTTG	960
TTGTTAGATG AGAAAACCTTC CTTGTCAGTC TGTCTCTACG ACTAGAATGG AAAGCCTTAC	1020
TACTTCCTAT GTATTCTTAA TATTTCAAAT GTCTAATTAA TGTTTGGCTT CTCTGTCTTT	1080
AAGGGATTAA GTCTCTGGAT TTGAAGAAAT AAATAAATAA ATAAAGGAAA ACTAATTTC	1140
TCGTGCCGGA TGACTGCTAG CTGAGCTCAG GCCTACTGCA TTCTACATTT CGACTCTCTC	1200
CCTCTTCCCC AGTGCTTAG CACTGGACTG GGCACTNCCT GGCCTGGTCT AACTCCTGTT	1260
TCCTGGTGGG AATGTATAAT AAGAACTCCA TGAGTTCTGG TATAAACACT GTGGTCTGTG	1320
TGCTAATTAA ATCTNGTGTGTT TCCTACAGCC CCTGACGAAA AATGACTCAC TGTGTAGTGT	1380
GAGGAGGTAC GTGGTGAAGC ATCGTACTGC CCACAATGGG ACGTGGTCAG AAGATGTGGG	1440
AAATCGGACC AATCTCACTT TCCTGTGGAC AGAACCAAGCG CACACTGTTA CAGTTCTGGC	1500
TGTCAATTCC CTCGGCGCTT CCCTTGTGAA TTTAACCTT ACCTTCTCAT GGCCCATGAG	1560
TAAAGTGAGT GCTGTGGAGT CACTCAGTGC TTATCCCTG AGCAGCAGCT GTGTCATCCT	1620
TTCCCTGGACA CTGTCACCTG ATGATTATAG TCTGTTATAT CTGGTTATTG AATGGAAGAT	1680
CCTTAATGAA GATGATGGAA TGAAGTGGCT TAGAATTCCC TCGAATGTTA AAAAGTTTA	1740
TATCCACGAT AATTTTATTC CCATCGAGAA ATATCAGTTT AGTCTTACCA CAGTATTAT	1800
GGAAGGAGTT GGAAAACCAA AGATAATTAA TGGTTTCACC AAAGATGCTA TCGACAAGCA	1860
GCAGAATGAC GCAGGGCTGT ATGTCATTGT ACCCATAATT ATTCCTCTT GTGTCCTACT	1920
GCTCGGAACA CTGTTAATTTC CACACCAGAG AATGAAAAAG TTGTTTGGG ACGATGTTCC	1980
AAACCCCAAG AATTGTTCCCT GGGCACAAAGG ACTGAATTTC CAAAGCCTG AAACATTGAA	2040
GCATCTTTT ACCAAGCATG CAGAATCAGT GATATTGGT CCTCTTCTTC TGGAGCCTGA	2100
ACCCATTCA GAAGAAATCA GTGTCGATAC AGCTGGAAA AATAAAGATG AGATGGTCCC	2160
AGCAGCTATG GTCTCCCTTC TTTGACCAC ACCAGACCCCT GAAAGCAGTT CTATTGTAT	2220
TAGTGACCAG TGTAACAGTG CTAACCTCTC TGGGTCTCAG AGCACCCAGG TAACCTGTGA	2280

GGATGAGTGT CAGAGACAAC CCTCAGTTAA ATATGCAACT CTGGTCAGCA ACGATAAACT	2340
AGTGGAAACT GATGAAGAGC AAGGGTTTAT CCATAGTCCT GTCAGCAACT GCATCTCCAG	2400
TAATCATTCC CCACTGAGGC AGTCTTCCTC TAGCAGCTCC TGGGAGACAG AGGCCAGAC	2460
ATTTTCCCTT TTATCAGACC AGCAACCCAC CATGATTCA CCACAACTTT CATTCTCGGG	2520
GTTGGATGAG CTTTGGAAC TGGAGGGAAG TTTCTGAA GAAAATCACA GGGAGAAGTC	2580
TGTCTGTTAT CTAGGAGTCA CCTCCGTCAA CAGAAGAGAG AGTGGTGTGC TTTTGACTGG	2640
TGAGGCAGGA ATCCTGTGCA CATTCCCAGC CCAGTGTCTG TTCAGTGACA TCAGGATCCT	2700
CCAGGAGAGA TGCTCACACT TTGTAGAAAA TAATTTGAGT TTAGGGACCT CTGGTGAGAA	2760
CTTTGTACCT TACATGCCCT AATTCAAAC CTGTTCCACG CACAGTCACA AGATAATGGA	2820
GAATAAGATG TGTGACTTAA CTGTGTAATC TCATCCAAGA AGCCTCAAGG TTCCATTCCA	2880
GTAGAGCCCTG TCATGTATAA TGTGTTCTTT ATTG	2914

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: QB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg Tyr Val Val
1 5 10 15

Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp Val Gly Asn
20 25 30

Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His Thr Val Thr
35 40 45

Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn Phe Asn Leu
50 55 60

Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu Ser Leu Ser
65 70 75 80

Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp Thr Leu Ser
85 90 95

Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp Lys Ile Leu
100 105 110

Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser Asn Val Lys
115 120 125

Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys Tyr Gln Phe
130 135 140

Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro Lys Ile Ile
145 150 155 160

Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn Asp Ala Gly
165 170 175

Leu Tyr Val Ile Val Pro Ile Ile Ser Ser Cys Val Leu Leu Leu
180 185 190

Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu Phe Trp Asp
195 200 205

Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly Leu Asn Phe
210 215 220

Gln Lys Pro Glu Thr Phe Glu His Leu Phe Thr Lys His Ala Glu Ser
225 230 235 240

Val Ile Phe Gly Pro Leu Leu Leu Glu Pro Glu Pro Ile Ser Glu Glu
245 250 255

Ile Ser Val Asp Thr Ala Trp Lys Asn Lys Asp Glu Met Val Pro Ala
260 265 270

Ala Met Val Ser Leu Leu Leu Thr Thr Pro Asp Pro Glu Ser Ser Ser
275 280 285

Ile Cys Ile Ser Asp Gln Cys Asn Ser Ala Asn Phe Ser Gly Ser Gln
290 295 300

Ser Thr Gln Val Thr Cys Glu Asp Glu Cys Gln Arg Gln Pro Ser Val
305 310 315 320

Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr Asp Glu
325 330 335

Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser Ser Asn
340 345 350

His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Trp Glu Thr Glu
355 360 365

Ala Gln Thr Phe Phe Leu Leu Ser Asp Gln Gln Pro Thr Met Ile Ser

370	375	380		
Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu Glu Gly				
385	390	395	400	
Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr Leu Gly				
405		410	415	
Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly Glu				
420		425	430	
Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp Ile				
435		440	445	
Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu Ser				
450		455	460	
Leu Gly Thr Ser Gly Glu Asn Phe Val Pro Tyr Met Pro Gln Phe Gln				
465		470	475	480
Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys Asp				
485		490	495	
Leu Thr Val				

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
CODING REGION: 272-958

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTGAGA AATAAATAAA TAAATAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT	180
GTTCCTGGT GGGAAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT	240

GTGTGCTAAT TAAATCTNGT GTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT	540
CCTTCCTGG ACACGTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT	660
TTATATCCAC GATAATTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT	720
TATGGAAGGA GTTGGAAAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA	780
GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTCCT CTTGTGTCCT	840
ACTGCTCGGA ACACGTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTTT GGGACGATGT	900
TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTA	960
AGTATTTAA CCCAGATATC TAAGGTTGCA GTT TAGATGC CACAGTACTT ACAGATCTTT	1020
AAACAACTTT AAAGGGCTTT ATGTTGTTGT GTTCATGTT CCAAGCCTGT TCATCCTTTC	1080
TCTTCTCAA AAGCTGGGTT TGGGATTGTA TCAGAGAAAA CAAAGTTCGC TCCCTTATCT	1140
CATGAGAGTT GACAACACAT CTATCTCTCT TTCTGCTTAC TGTACATAAA AAAAATAAAAT	1200
ACTACAAGAG GAAGGAATGT TATAGATGGA GAATAGATAG	1240

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val
1				5					10				15		
Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn
				20				25					30		
Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr
			35			40						45			
Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu
			50			55				60					
Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser
			65			70			75				80		
Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	Thr	Leu	Ser
			85					90				95			
Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	Lys	Ile	Leu
			100					105				110			
Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	Asn	Val	Lys
			115					120				125			
Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	Tyr	Gln	Phe
			130				135				140				
Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	Lys	Ile	Ile
			145			150			155				160		
Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	Asp	Ala	Gly
			165					170				175			
Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	Leu	Leu	Leu
			180					185				190			
Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp
			195					200				205			
Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly	Leu	Asn	Phe
			210					215				220			
Gln	Lys	Val	Thr	Val											
			225												

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2892 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - CODING REGION: 1-2700

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC AGAAATTCTA TGTGGTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACCTAACCC TGGCATATCC AATCTCTCCC TGGAAATTAA AGTTGTTTG TGGACCACCG	120
AACACAAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTG	180
AAGGGGGCTT CTGAAGCAAT TGTTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCCCT	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AACTGCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTGCGCTC TGCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTG TGAAACCCGA TCCACCCCTTA	720
GGTTTGCATA TGGAAAGTCAC AGATGATGGT AATTAAAGA TTTCTTGGGA CAGCCAAACA	780
ATGGCACCAC TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA	840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT	900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG	960
AGTTCACCTC AAGTCTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT	1020
AGTGTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC	1080
TCAAAACAGA TAGTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC	1140
ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA	1200
GGGAAGTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCAGGCCA TCACCGCTAT	1260
GCTGAATTAT ACGTGATCGA TGTCAATATC AATATATCAT GTGAAACTGA CGGGTACTTA	1320
ACTAAAATGA CTTGCAGATG GTCACCCAGC ACAATCCAAT CACTAGTGGG AAGCACTGTG	1380

CAGCTGAGGT ATCACAGGCG CAGCCTGTAT TGTCTGATA GTCCATCTAT TCATCCTACG	1440
TCTGAGCCCA AAAACTGCGT CTTACAGAGA GACGGCTTT ATGAATGTGT TTTCCAGCCA	1500
ATCTTCTAT TATCTGGCTA TACAATGTGG ATCAGGATCA ACCATTCTT AGGTTCACTT	1560
GACTCGCCAC CAACGTGTGT CCTTCCTGAC TCCGTAGTAA AACCACTACC TCCATCTAAC	1620
GTAAAAGCAG AGATTACTGT AAACACTGGA TTATTGAAAG TATCTTGGGA AAAGCCAGTC	1680
TTTCCGGAGA ATAACCTTCA ATTCCAGATT CGATATGGCT TAAGTGGAAA AGAAATACAA	1740
TGGAAGACAC ATGAGGTATT CGATGCAAAG TCAAAGTCTG CCAGCCTGCT GGTGTCAGAC	1800
CTCTGTGCAG TCTATGTGGT CCAGGTTCGC TGCCGGCGGT TGGATGGACT AGGATATTGG	1860
AGTAATTGGA GCAGTCCAGC CTATACGCTT GTCATGGATG TAAAAGTTCC TATGAGAGGG	1920
CCTGAATTTT GGAGAAAAAT GGATGGGGAC GTTACTAAA AGGAGAGAAA TGTCACCTTG	1980
CTTTGGAAGC CCCTGACGAA AAATGACTCA CTGTGTAGTG TGAGGAGGTA CGTGGTGAAG	2040
CATCGTACTG CCCACAATGG GACGTGGTCA GAAGATGTGG GAAATCGGAC CAATCTCACT	2100
TTCCTGTGGA CAGAACCAAGC GCACACTGTT ACAGTTCTGG CTGTCAATTG CCTCGGCGCT	2160
TCCCTTGTGA ATTTAACCT TACCTTCTCA TGGCCCATGA GTAAAGTGAG TGCTGTGGAG	2220
TCACTCAGTG CTTATCCCCT GAGCAGCAGC TGTGTCATCC TTTCCTGGAC ACTGTCACCT	2280
GATGATTATA GTCTGTTATA TCTGGTTATT GAATGGAAGA TCCTTAATGA AGATGATGGA	2340
ATGAAGTGGC TTAGAATTCC CTCGAATGTT AAAAAGTTT ATATCCACGA TAATTTATT	2400
CCCATCGAGA AATATCAGTT TAGTCTTAC CCAGTATTTA TGGAAGGAGT TGAAAACCA	2460
AAGATAATTAA ATGGTTTCAC CAAAGATGCT ATCGACAAGC AGCAGAATGA CGCAGGGCTG	2520
TATGTCATTG TACCCATAAT TATTCCTCT TGTGTCCTAC TGCTCGGAAC ACTGTTAATT	2580
TCACACCAGA GAATGAAAAA GTTGGTTGG GACGATGTTG CAAACCCCAA GAATTGTTCC	2640
TGGGCACAAG GACTGAATTG CCAAAAGGAT ATATCTTAC ATGAAGTTT TATTTTCAGA	2700
TAGCCTCTGG CAGATTCTCA CTGTGGCCTG AGGCAGCCTG AAACATTGA GCATTTTTT	2760
ACCAAGCATG CAGAACAGT GATATTGGT CCTCTTCTTC TGGAGCCTGA ACCCATTCA	2820
GAAGAAATCA GTGTCGATAC AGCTTGGAAA AATAAAGATG AGATGGTCCC AGCAGCTATG	2880
GTCTCCCTTC TT	2892

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
35 40 45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
50 55 60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65 70 75 80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
85 90 95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
100 105 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
115 120 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
130 135 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
145 150 155 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
165 170 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
180 185 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
195 200 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
290 295 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
305 310 315 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
325 330 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
355 360 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
370 375 380

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
385 390 395 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
405 410 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
420 425 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
435 440 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465 470 475 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
485 490 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
500 505 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
515 520 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
530 535 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
545 550 555 560

Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
565 570 575

Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
580 585 590

Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
595 600 605

Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
610 615 620

Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625 630 635 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
645 650 655

Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
660 665 670

Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
675 680 685

Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
690 695 700

Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
705 710 715 720

Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
725 730 735

Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
740 745 750

Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
755 760 765

Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
770 775 780

Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
785 790 795 800

Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
805 810 815

Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp

820	825	830
Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile		
835	840	845
Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg		
850	855	860
Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser		
865	870	875
Trp Ala Gln Gly Leu Asn Phe Gln Lys Asp Ile Ser Leu His Glu Val		
885	890	895
Phe Ile Phe Arg		
900		

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - CODING REGION: 1-2415
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGATGTGTC AGAAATTCTA TGTGGTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACCTAACCC TGGCATATCC AATCTCTCCC TGGAAATTAA AGTTGTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCCCT	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAACTGCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTCGCCTC TGCCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600

AGAGCCAAAC	TCAACTACGC	TCTTCTGATG	TATTGGAAA	TCACATCTGC	CGGTGTGAGT	660
TTTCAGTCAC	CTCTGATGTC	ACTGCAGCCC	ATGCTTGGT	TGAAACCCGA	TCCACCCCTTA	720
GGTTTGCATA	TGGAAGTCAC	AGATGATGGT	AATTAAAGA	TTTCTTGGGA	CAGCCAAACAA	780
ATGGCACCAT	TTCCGCTTCA	ATATCAGGTG	AAATATTTAG	AGAATTCTAC	AATTGTAAGA	840
GAGGCTGCTG	AAATTGTCTC	AGCTACATCT	CTGCTGGTAG	ACAGTGTGCT	TCCTGGATCT	900
TCATATGAGG	TCCAGGTGAG	GAGCAAGAGA	CTGGATGGTT	CAGGAGTCTG	GAGTGACTGG	960
AGTTCACCTC	AAGTCTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTGGAT	CGAATGCTTC	TTTCATTGC	ATCTACAAAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTGGTG	GAGGAATCTA	GCTGAGAAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTA	CCTATGACGC	AGTGTACTGC	TGCAATGAGC	AGGCCTGCCA	TCACCGCTAT	1260
GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCA	AAAACCTGCGT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACTT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTTGGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGGAAA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTCAAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTCGC	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTCTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCCTGTGGA	CAGAACCAAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTC	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGTAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGTCACTCC	TTTCCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340

ATGAAAGTGGC TTAGAATTCC CTCGAATGTT AAAAAGTTT ATATCCACGG TATGTGTACT	2400
GTACTTTCA TGGATTAGTA TGACACTGTA GACTGGCAAT TCTGATAATA AATCATTAA	2460
TGACAAACC	2468

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 805 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
35 40 45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
50 55 60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65 70 75 80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
85 90 95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
100 105 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
115 120 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
130 135 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His

145	150	155	160
Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro			
165	170	175	
Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly			
180	185	190	
Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu			
195	200	205	
Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro			
210	215	220	
Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu			
225	230	235	240
Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp			
245	250	255	
Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr			
260	265	270	
Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala			
275	280	285	
Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val			
290	295	300	
Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp			
305	310	315	320
Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro			
325	330	335	
Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr			
340	345	350	
Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg			
355	360	365	
Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp			
370	375	380	
Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg			
385	390	395	400
Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys			
405	410	415	
His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile			
420	425	430	
Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser			
435	440	445	

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465 470 475 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
485 490 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
500 505 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
515 520 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
530 535 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
545 550 555 560

Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
565 570 575

Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
580 585 590

Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
595 600 605

Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
610 615 620

Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625 630 635 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
645 650 655

Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
660 665 670

Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
675 680 685

Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
690 695 700

Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
705 710 715 720

Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
725 730 735

Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
740 745 750

Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu

755 760 765
Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
770 775 780
Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Gly Met Cys Thr
785 790 795 800
Val Leu Phe Met Asp
805

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Phe Gln Lys Arg Thr Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn Phe Gln Lys Pro Glu Thr Phe Glu Gln Leu Phe Thr Lys His Ala
1 5 10 15

Glu Ser Val Ile Phe Gly Pro Leu Leu Leu Glu Pro Glu Pro Ile Ser
20 25 30

Glu Glu Ile Ser Val Asp Thr Ala Trp Lys Asn Lys Asp Glu Met Val
35 40 45

Pro Ala Ala Met Val Ser Leu Leu Trp Thr Thr Pro Asp Pro Glu Ser
50 55 60

Ser Ser Ile Cys Ile Ser Asp Gln Cys Asn Ser Ala Asn Phe Ser Gly
65 70 75 80

Ser Gln Ser Thr Gln Val Cys Glu Asp Glu Cys Gln Arg Gln Pro Ser
85 90 95

Val Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr Asp
100 105 110

Glu Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser Ser
115 120 125

Asn His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Trp Glu Thr
130 135 140

Glu Ala Gln Thr Phe Phe Leu Leu Ser Asp Gln Gln Pro Thr Met Ile
145 150 155 160

Ser Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu Glu
165 170 175

Gly Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr Leu
180 185 190

Gly Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly
195 200 205

Glu Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp
210 215 220

Ile Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu
225 230 235 240

Ser Leu Gly Thr Ser Gly Glu Asn Phe Gly Pro Tyr Met Pro Gln Phe
245 250 255

Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys
260 265 270

Asp Phe Thr Val
275

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Phe Gln Lys Val Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Phe Gln Lys Asp Ile Ser His Glu Val Phe Ile Phe Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Tyr Ile His Gly Met Cys Thr Val Leu Phe Met Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACCC TTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
1 5 10 15

Ser Glu Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Arg Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn
1 5 10 15

Cys Ser Trp

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAACA GTGTGCGCTG GTTCTGTCCA	60
CAGGAAAGTG AGATTGGTCC GATTTCACAC ATCTTCTGAC CACGTCCCAT TGTGGCAGT	120
ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT	166

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCA ACAATGGGAC GTGGTCAGAA GATGTGGAA ATCGGACCAA	60
TCTCACTTTC CTGTGGACAG AACCAAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCCT	120
CGCGCGTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA	320

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT	120
CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG	158

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTCATT TGATGTTCA	60
AAGTCAGCAA GGTTCTCATA TGTCCCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG	120
CTAACAAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACAC TACTTG GTGTTTTACT	180
TAAAGATAACG AG	192

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTC TCATCTAAC	AGCAAGCAAA GGAAGTGCTT ATGTNCTGTG	60
ANGAACCAAG GNAGCTCAGA TGTCACCATA	GTCATCATGA ACTCGAGTGA CTCTGCCACT	120
GTTCCCCCAG GATGTGCTTG GANGATAATC	CTGCGCAAGA AACAGATA	168

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATTTTAT ATGATCTGCC	TGAAGTCATA GATGATTGCG	60
CTCTGCCCTT	ACTGAAAGAC AGNTTCAGA CTGTCCAATG	120
GTGAATGTCA	TGTGCCAGTA CCCAGAGCCA AACTCAACTA	180
NAATCACATC	CGCTCTTCTG ATGTATTTGG	240
TTGTGAAACC	TGCCGGTGTG AGTTTCAGT CACCTCTGAT	259
CGATCCACC	GTCACTGCAG CCCATGCTTG	

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTGGG GCTCCAGCAG	60
GTGAGAGAAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACTTA AATTTCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAAACA	180
AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTCAG	240
AACGATTCCCT	250

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC	18
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(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG

22

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTTCCCTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATT CGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCACTG

20